

Abstract:

Metabolic network reconstruction of the central carbon metabolism of *Enterococcus faecalis*

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The profound advance in experimental high throughput techniques (generally referred to as “omics techniques”) has enabled the analysis of a large number of components within a living cell. The vast amount of data obtained from the different “omics” (genomics, proteomics, fluxomics, metabolomics, transcriptomics) demands the use of bioinformatics tools. These methods comprise the development of comparative tools and maintenance of databases for the analysis of genomics data, in addition to the construction of models for the analysis and integration of data in a system-wide approach. *Enterococcus faecalis* is a Gram-positive bacterium that is getting more attention due to its “two-face” behavior. This natural inhabitant of the mammalian gastrointestinal tract is also an opportunist pathogen responsible for urinary tract infections, nosocomial infections, bacteremia and infective endocarditis. Besides, its intrinsic physiological properties such as inherent antibiotic resistance and exceptional ability to adapt to harsh conditions provide this organism with an enormous advantage in the infection processes. Here, we propose to reconstruct the genome scale metabolic network of the central carbon metabolism of *Enterococcus faecalis* using genome sequencing information available on different databases as well as proteomics and metabolomics data. The first metabolic model generated for this bacterium will allow correlating metabolite levels and fluxes which enables identification of key control points in its metabolism. As it has been previously shown for other organisms, the metabolic network reconstruction may serve as a valuable tool to predict the phenotypic behaviour under various genetic and environmental conditions.